

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2005, 12:16:33 ; Search time 124 Seconds
(without alignments)
368.046 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGGLVQPSQSL SIT.....SYPYNYFDVWGQGT TTVTSA 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	638	100.0	118	8	ADQ98036	Adq98036 Mutant mu
2	638	100.0	120	8	ADQ98119	Adq98119 Murine 2D
3	638	100.0	227	8	ADQ98061	Adq98061 Chimeric
4	638	100.0	254	8	ADQ98106	Adq98106 Chimeric
5	626	98.1	118	8	ADQ98034	Adq98034 Mutant mu
6	626	98.1	120	8	ADQ98117	Adq98117 Murine 2D
7	626	98.1	227	8	ADQ98059	Adq98059 Chimeric
8	626	98.1	254	8	ADQ98104	Adq98104 Chimeric
9	621	97.3	118	8	ADQ98033	Adq98033 Cloned hy

10	621	97.3	120	8	ADQ98116	Adq98116	Murine 2D
11	621	97.3	227	8	ADQ98058	Adq98058	Chimeric
12	621	97.3	227	8	ADQ98063	Adq98063	Chimeric
13	621	97.3	254	8	ADQ98103	Adq98103	Chimeric
14	621	97.3	254	8	ADQ98108	Adq98108	Chimeric
15	618	96.9	118	8	ADQ98109	Adq98109	Native hy
16	618	96.9	118	8	ADQ98064	Adq98064	Native hy
17	618	96.9	118	8	ADQ98032	Adq98032	Native hy
18	618	96.9	119	8	ADQ98028	Adq98028	Murine an
19	617	96.7	118	8	ADQ98035	Adq98035	Mutant mu
20	617	96.7	118	8	ADQ98037	Adq98037	Mutant mu
21	617	96.7	120	8	ADQ98120	Adq98120	Murine 2D
22	617	96.7	120	8	ADQ98118	Adq98118	Murine 2D
23	617	96.7	227	8	ADQ98062	Adq98062	Chimeric
24	617	96.7	227	8	ADQ98060	Adq98060	Chimeric
25	617	96.7	254	8	ADQ98105	Adq98105	Chimeric
26	617	96.7	254	8	ADQ98107	Adq98107	Chimeric
27	499	78.2	264	2	AAR95570	Aar95570	Intracell
28	498.5	78.1	116	8	ADQ91072	Adq91072	Anti EpCA
29	498.5	78.1	492	8	ADQ91080	Adq91080	Antibody
30	498.5	78.1	492	8	ADQ91090	Adq91090	Antibody
31	498.5	78.1	492	8	ADQ91082	Adq91082	Antibody
32	498.5	78.1	492	8	ADQ91084	Adq91084	Antibody
33	498.5	78.1	492	8	ADQ91104	Adq91104	Antibody
34	498.5	78.1	492	8	ADQ91106	Adq91106	Antibody
35	498.5	78.1	492	8	ADQ91088	Adq91088	Antibody
36	498.5	78.1	492	8	ADQ91086	Adq91086	Antibody
37	498.5	78.1	492	8	ADQ91092	Adq91092	Antibody
38	498.5	78.1	492	8	ADQ91094	Adq91094	Antibody
39	498.5	78.1	492	8	ADQ91100	Adq91100	Antibody
40	498.5	78.1	492	8	ADQ91096	Adq91096	Antibody
41	498.5	78.1	492	8	ADQ91098	Adq91098	Antibody
42	498.5	78.1	492	8	ADQ91102	Adq91102	Antibody
43	498.5	78.1	492	8	ADQ91078	Adq91078	Bispecifi
44	497.5	78.0	450	3	AAY44991	Aay44991	M79scFv-i
45	497.5	78.0	451	8	ADR43339	Adr43339	scFv anti

ALIGNMENTS

RESULT 1

ADQ98036

ID ADQ98036 standard; protein; 118 AA.

XX

AC ADQ98036;

XX

DT 21-OCT-2004 (first entry)

XX

DE Mutant murine antibody 2D12.5 variable heavy chain protein N87D G54C.

XX

KW murine; mouse; mutant; mutein; antigen recognition domain;

KW in vivo imaging; cell-antibody-metal chelate complex;

KW emission tomography; magnetic resonance imaging; lanthanide luminescence;

KW gamma-emissions; single photon emission tomography; SPET; cancer;

KW cytostatic; immunosuppressive; multi-functional antibody; metal chelate.

XX

OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 54
FT /note= "Wild type Gly substituted for Cys"
FT Misc-difference 87
FT /note= "Wild type Asn substituted for Asp"
XX
PN WO2004065569-A2.
XX
PD 05-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001808.
XX
PR 23-JAN-2003; 2003US-00350555.
PR 22-JUL-2003; 2003US-00625047.
PR 31-JUL-2003; 2003US-00631258.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Corneillie T;
XX
DR WPI; 2004-580725/56.
DR N-PSDB; ADQ98042.
XX
PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.
XX
PS Claim 41; SEQ ID NO 13; 208pp; English.
XX
CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody
CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polypeptide sequence is
CC a mutant murine antibody 2D12.5 variable heavy chain protein of the
CC invention.
XX
SQ Sequence 118 AA;

PT autoimmune diseases.

XX

PS Disclosure; SEQ ID NO 96; 208pp; English.

XX

CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody
CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polypeptide sequence is
CC a mutant murine 2D12.5 antibody IgG1 heavy chain variable domain protein,
CC given in an exemplification of the invention.

XX

SQ Sequence 120 AA;

Query Match 100.0%; Score 638; DB 8; Length 120;

Best Local Similarity 100.0%; Pred. No. 9.7e-55;

Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLQESGPGGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVWISGCGTAYTA 60

|||||

Db 3 VKLQESGPGGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVWISGCGTAYTA 62

Qy 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGT TVTVSA 118

|||||

Db 63 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGT TVTVSA 120

RESULT 3

ADQ98061

ID ADQ98061 standard; protein; 227 AA.

XX

AC ADQ98061;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric murine N87D G54C 2D12.5 VH antibody fused to human TTCH protein.

XX

KW murine; mouse; chimeric; human; TTCH; tetanus toxin;

KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;

KW single photon emission tomography; SPET; cancer; cytostatic;

KW immunosuppressive; multi-functional antibody; metal chelate;

KW antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography; mutant; mutein.

XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Chimeric.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 54
 FT /note= "Wild type Gly substituted for Cys"
 FT Misc-difference 87
 FT /note= "Wild type Asn substituted for Asp"
 XX
 PN WO2004065569-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 23-JAN-2004; 2004WO-US001808.
 XX
 PR 23-JAN-2003; 2003US-00350555.
 PR 22-JUL-2003; 2003US-00625047.
 PR 31-JUL-2003; 2003US-00631258.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR N-PSDB; ADQ98068.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 41; SEQ ID NO 38; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polypeptide sequence is
 CC the chimeric mutant N87D G54C murine antibody 2D12.5 variable heavy chain
 CC protein fused to the human anti-tetanus toxin antibody CH1 heavy chain

CC constant region of the invention.

XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 638; DB 8; Length 227;
Best Local Similarity 100.0%; Pred. No. 2e-54;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
|||||

Db 3 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 62

Qy 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSPYNYFDVWGQGT TVTVSA 118
|||||

Db 63 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSPYNYFDVWGQGT TVTVSA 120

RESULT 4

ADQ98106

ID ADQ98106 standard; protein; 254 AA.

XX

AC ADQ98106;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric 2dVH-TTCH protein with tag and an N87D/G54C mutations SeqID 84.

XX

KW murine; mouse; chimeric; human; TTCH; tetanus toxin;

KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;

KW single photon emission tomography; SPET; cancer; cytostatic;

KW immunosuppressive; multi-functional antibody; metal chelate;

KW antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography; V5 epitope;

KW His tag; mutant; mutein.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 54

FT /note= "Wild type Gly substituted for Cys"

FT Misc-difference 87

FT /note= "Wild type Asn substituted for Asp"

XX

PN WO2004065569-A2.

XX

PD 05-AUG-2004.

XX

PF 23-JAN-2004; 2004WO-US001808.

XX

PR 23-JAN-2003; 2003US-00350555.

PR 22-JUL-2003; 2003US-00625047.

PR 31-JUL-2003; 2003US-00631258.

XX

PA (REGC) UNIV CALIFORNIA.

XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR N-PSDB; ADQ98099.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 41; SEQ ID NO 83; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polypeptide is the
 CC mutant protein sequence comprising a chimeric murine antibody 2D12.5
 CC variable heavy chain protein fused to the human anti-tetanus toxin
 CC antibody CH1 heavy chain constant region (2dVH-TTCH) with N87D and G54C
 CC mutations and a V5 epitope with (His)6 tag, given in an exemplification
 CC of the invention.
 XX
 SQ Sequence 254 AA;

Query Match 100.0%; Score 638; DB 8; Length 254;
 Best Local Similarity 100.0%; Pred. No. 2.2e-54;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLQESGPGVLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVWISGCGTAYTA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3 VKLQESGPGVLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVWISGCGTAYTA 62
 Qy 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMY YCARRGSYPNYFDVWGQGT TTVTVSA 118
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 63 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMY YCARRGSYPNYFDVWGQGT TTVTVSA 120

RESULT 5
 ADQ98034
 ID ADQ98034 standard; protein; 118 AA.
 XX

AC ADQ98034;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Mutant murine antibody 2D12.5 variable heavy chain protein N87D Seq 11.
 XX
 KW murine; mouse; mutant; mutein; antigen recognition domain;
 KW in vivo imaging; cell-antibody-metal chelate complex;
 KW emission tomography; magnetic resonance imaging; lanthanide luminescence;
 KW gamma-emissions; single photon emission tomography; SPET; cancer;
 KW cytostatic; immunosuppressive; multi-functional antibody; metal chelate.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 87
 FT /note= "Wild type Asn substituted for Asp"
 XX
 PN WO2004065569-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 23-JAN-2004; 2004WO-US001808.
 XX
 PR 23-JAN-2003; 2003US-00350555.
 PR 22-JUL-2003; 2003US-00625047.
 PR 31-JUL-2003; 2003US-00631258.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR N-PSDB; ADQ98040.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 41; SEQ ID NO 11; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex

us-10-631-258-13.rapb

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2005, 15:39:42 ; Search time 1892 Seconds
(without alignments)
23.908 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGLVQPSQSLSIT.....SYPYNYFDVWGQGTTTVSA 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	638	100.0	118	16	US-10-625-047-13	Sequence 13, Appl

				us-10-631-258-13.rapb		
2	638	100.0	118	17	US-10-631-258-13	Sequence 13, Appl
3	638	100.0	227	16	US-10-625-047-38	Sequence 38, Appl
4	638	100.0	227	17	US-10-631-258-38	Sequence 38, Appl
5	626	98.1	118	16	US-10-625-047-11	Sequence 11, Appl
6	626	98.1	118	17	US-10-631-258-11	Sequence 11, Appl
7	626	98.1	227	16	US-10-625-047-36	Sequence 36, Appl
8	626	98.1	227	17	US-10-631-258-36	Sequence 36, Appl
9	621	97.3	118	16	US-10-625-047-10	Sequence 10, Appl
10	621	97.3	118	17	US-10-631-258-10	Sequence 10, Appl
11	621	97.3	227	16	US-10-625-047-35	Sequence 35, Appl
12	621	97.3	227	16	US-10-625-047-40	Sequence 40, Appl
13	621	97.3	227	17	US-10-631-258-35	Sequence 35, Appl
14	621	97.3	227	17	US-10-631-258-40	Sequence 40, Appl
15	618	96.9	118	16	US-10-625-047-9	Sequence 9, Appli
16	618	96.9	118	16	US-10-625-047-41	Sequence 41, Appl
17	618	96.9	118	17	US-10-631-258-9	Sequence 9, Appli
18	618	96.9	118	17	US-10-631-258-41	Sequence 41, Appl
19	618	96.9	119	16	US-10-625-047-5	Sequence 5, Appli
20	618	96.9	119	17	US-10-631-258-5	Sequence 5, Appli
21	617	96.7	118	16	US-10-625-047-12	Sequence 12, Appl
22	617	96.7	118	16	US-10-625-047-14	Sequence 14, Appl
23	617	96.7	118	17	US-10-631-258-12	Sequence 12, Appl
24	617	96.7	118	17	US-10-631-258-14	Sequence 14, Appl
25	617	96.7	227	16	US-10-625-047-37	Sequence 37, Appl
26	617	96.7	227	16	US-10-625-047-39	Sequence 39, Appl
27	617	96.7	227	17	US-10-631-258-37	Sequence 37, Appl
28	617	96.7	227	17	US-10-631-258-39	Sequence 39, Appl
29	607	95.1	116	17	US-10-854-735-13	Sequence 13, Appl
30	607	95.1	116	17	US-10-835-533-13	Sequence 13, Appl
31	595	93.3	116	17	US-10-854-735-11	Sequence 11, Appl
32	595	93.3	116	17	US-10-835-533-11	Sequence 11, Appl
33	590	92.5	116	17	US-10-854-735-10	Sequence 10, Appl
34	590	92.5	116	17	US-10-835-533-10	Sequence 10, Appl
35	587	92.0	116	17	US-10-854-735-9	Sequence 9, Appli
36	587	92.0	116	17	US-10-835-533-9	Sequence 9, Appli
37	587	92.0	117	17	US-10-854-735-5	Sequence 5, Appli
38	587	92.0	117	17	US-10-835-533-5	Sequence 5, Appli
39	586	91.8	116	17	US-10-854-735-12	Sequence 12, Appl
40	586	91.8	116	17	US-10-854-735-14	Sequence 14, Appl
41	586	91.8	116	17	US-10-835-533-12	Sequence 12, Appl
42	586	91.8	116	17	US-10-835-533-14	Sequence 14, Appl
43	498.5	78.1	116	16	US-10-682-845-53	Sequence 53, Appl
44	498.5	78.1	492	16	US-10-682-845-59	Sequence 59, Appl
45	498.5	78.1	492	16	US-10-682-845-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1

US-10-625-047-13

; Sequence 13, Application US/10625047

; Publication No. US20040198962A1

GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

Db 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTDTVSA 118

RESULT 3

US-10-625-047-38

; Sequence 38, Application US/10625047
 ; Publication No. US20040198962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meares, Claude
 ; APPLICANT: Corneillie, Todd
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Multi-Functional Antibodies
 ; FILE REFERENCE: 023070-130910US
 ; CURRENT APPLICATION NUMBER: US/10/625,047
 ; CURRENT FILING DATE: 2003-07-22
 ; PRIOR APPLICATION NUMBER: US 10/350,555
 ; PRIOR FILING DATE: 2003-01-23
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 38
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C
 ; OTHER INFORMATION: cloned mutant chimeric murine 2D12.5 heavy chain
 ; OTHER INFORMATION: variable region (VH) fused to human anti-tetanus
 ; OTHER INFORMATION: toxin antibody CH1 heavy chain constant region
 ; OTHER INFORMATION: (TTCH)

US-10-625-047-38

Query Match 100.0%; Score 638; DB 16; Length 227;
 Best Local Similarity 100.0%; Pred. No. 9.4e-53;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGV IWSGCGTAYTA 60
 |||
 Db 3 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGV IWSGCGTAYTA 62
 Qy 61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTDTVSA 118
 |||
 Db 63 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSYPYNYFDVWGQGTDTVSA 120

RESULT 4

US-10-631-258-38

; Sequence 38, Application US/10631258
 ; Publication No. US20050026263A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meares, Claude
 ; APPLICANT: Corneillie, Todd
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Multi-Functional Antibodies
 ; FILE REFERENCE: 023070-130920US
 ; CURRENT APPLICATION NUMBER: US/10/631,258
 ; CURRENT FILING DATE: 2003-07-31
 ; PRIOR APPLICATION NUMBER: US 10/350,555
 ; PRIOR FILING DATE: 2003-01-23
 ; PRIOR APPLICATION NUMBER: US 10/625,047
 ; PRIOR FILING DATE: 2003-07-22
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 38

us-10-631-258-13.rapb

Query Match 100.0%; Score 638; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.4e-53;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

Query Match 98.1%; Score 626; DB 16; Length 118;
Best Local Similarity 99.2%; Pred. No. 6.5e-52;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2005, 15:15:54 ; Search time 41 Seconds
(without alignments)
276.917 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGGLVQPSQSL SIT.....SYPYNYFDVWGQGT TTVTVSA 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		Query		DB	ID	Description
		Match	Length	Match	Length			
1	496.5	77.8	135	2	S31913			Ig gamma-2A chain
2	487	76.3	127	2	B31807			Ig heavy chain V r
3	480	75.2	140	2	S14238			Ig gamma-1 chain p
4	479	75.1	114	2	S26321			Ig heavy chain V r
5	472.5	74.1	115	2	S26470			Ig heavy chain V r
6	466	73.0	121	2	D30560			Ig heavy chain V r
7	462	72.4	121	2	S33131			Ig heavy chain V r
8	458	71.8	115	2	S11107			Ig heavy chain V r
9	453	71.0	140	2	S55028			Ig heavy chain V r
10	452	70.8	116	2	PL0198			anti-DNA autoantib
11	452	70.8	118	2	PQ0266			Ig heavy chain V r
12	450.5	70.6	116	2	S42484			Ig heavy chain V r
13	450.5	70.6	117	2	S38563			Ig heavy chain V r

14	449	70.4	109	2	PH1026	Ig heavy chain V r
15	448	70.2	112	2	S11100	Ig heavy chain V r
16	448	70.2	231	2	PC4155	Ig gamma-2b chain
17	447	70.1	114	2	S11106	Ig heavy chain V r
18	446.5	70.0	122	2	A49049	Ig heavy chain V r
19	446	69.9	116	2	S11102	Ig heavy chain V r
20	444.5	69.7	139	2	A32456	Ig heavy chain pre
21	444	69.6	113	2	S11101	Ig heavy chain V r
22	440.5	69.0	141	2	S52446	Ig heavy chain V r
23	436	68.3	116	2	A33932	Ig mu chain precu
24	433.5	67.9	118	2	S32786	Ig heavy chain (an
25	433.5	67.9	120	2	PL0087	Ig heavy chain V r
26	433	67.9	115	2	S11103	Ig heavy chain V r
27	433	67.9	116	1	G1MS10	Ig heavy chain pre
28	432	67.7	106	2	S26322	Ig heavy chain V r
29	431.5	67.6	122	2	S20809	Ig heavy chain V r
30	431	67.6	100	2	A25913	Ig heavy chain pre
31	431	67.6	114	2	S11099	Ig heavy chain V r
32	429	67.2	112	2	S11108	Ig heavy chain V r
33	425	66.6	90	2	A49042	Ig heavy chain V r
34	425	66.6	144	1	G2MS14	Ig heavy chain pre
35	418.5	65.6	107	2	S14506	Ig heavy chain V r
36	418.5	65.6	144	2	S11244	Ig gamma-2a chain
37	417	65.4	114	2	S11105	Ig heavy chain V r
38	412	64.6	117	2	S10111	Ig heavy chain V r
39	411	64.4	112	2	S11098	Ig heavy chain V r
40	411	64.4	114	2	S11104	Ig heavy chain V r
41	410.5	64.3	107	2	S14492	Ig heavy chain V r
42	407	63.8	106	2	S14489	Ig heavy chain V r
43	407	63.8	111	2	S26324	Ig heavy chain V r
44	406.5	63.7	107	2	S14493	Ig heavy chain V r
45	405.5	63.6	107	2	S14491	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S31913

Ig gamma-2A chain precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999

C;Accession: S31913

R;Bespalov, I.A.; Hiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponova, G.I.; Deyev, S.M.

submitted to the EMBL Data Library, January 1993

A;Reference number: S31913

A;Accession: S31913

A;Molecule type: mRNA

A;Residues: 1-135 <BES>

A;Cross-references: EMBL:X70822; NID:g57921; PIDN:CAA50153.1; PID:g57922

A;Experimental source: strain BALB/c

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-11/Domain: signal sequence #status predicted <SIG>

F;12-135/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>

F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 496.5; DB 2; Length 135;
 Best Local Similarity 80.5%; Pred. No. 3.6e-40;
 Matches 95; Conservative 10; Mismatches 10; Indels 3; Gaps 1;

```

Qy      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
          |:::||||||||||||||||||||| ||||||||||||||||||| | | |
Db      21 VQLKQSGPGLVQPSQSL SITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGSTDYNA 80

Qy      61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARRGSPYNYFDVWGQGT TVTVSA 118
          |||||:| ||||:||||:||||:||||:|||| | || |||||:|:|
Db      81 AFISRLSISKDNSKSQVFFKMNSLQANDTAIYYCARELVY---YFDYWGQGTTLTVSS 135
  
```

RESULT 2

B31807

Ig heavy chain V region (PAC1) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 23-May-1997

C;Accession: B31807

R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shattil, S.J.

J. Biol. Chem. 264, 259-265, 1989

A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequence that mimics a receptor recognition domain in fibrinogen.

A;Reference number: A31807; MUID:89079661; PMID:2909518

A;Accession: B31807

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-127 <TAU>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 487; DB 2; Length 127;
 Best Local Similarity 74.6%; Pred. No. 2.7e-39;
 Matches 94; Conservative 11; Mismatches 13; Indels 8; Gaps 1;

```

Qy      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
          |:|::| ||||||||||||||||||| ||||||| ||||||||||| | | |
Db      2 VQLKQSGPGLVQPSQSL SITCTVSGFSLTSYGVHWVRLSPGKGLEWLGVIWSGGSTDYNA 61

Qy      61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYYCARR-----GSYPYNYFDVWGQGT 112
          |||||:| ||||:||||:||||:||||:| | :||| | | | ||||
Db      62 AFISRLSISKDNSKSQVFFKMNSLQANDTGIYYCARRSPSYRYDGAGPYYAMDYWGQGT 121

Qy      113 TVTVSA 118
          :|||:
Db      122 SVTVSS 127
  
```

us-10-631-258-13.rup

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2005, 13:18:42 ; Search time 123 Seconds
(without alignments)
491.263 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGLVQPSQSLSIT.....SYPYNYFDVWGQGTTVTVSA 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	433	67.9	116	1	HV45_MOUSE	P01821 mus musculu
2	425	66.6	144	1	HV43_MOUSE	P01819 mus musculu
3	423.5	66.4	121	2	Q99NG4	Q99ng4 mus musculu
4	417.5	65.4	482	2	Q91X92	Q91x92 mus musculu
5	378	59.2	115	1	HV44_MOUSE	P01820 mus musculu
6	374.5	58.7	135	1	HV02_XENLA	P20957 xenopus lae
7	359.5	56.3	573	2	Q8WU38	Q8wu38 homo sapien
8	358	56.1	472	2	Q6N089	Q6n089 homo sapien
9	348.5	54.6	136	1	HV16_MOUSE	P01783 mus musculu
10	348	54.5	119	2	Q9UL73	Q9ul73 homo sapien
11	347.5	54.5	613	2	Q8WUK1	Q8wuk1 homo sapien
12	341	53.4	476	2	Q6GMX1	Q6gmx1 homo sapien
13	336	52.7	492	2	Q7Z374	Q7z374 homo sapien
14	335.5	52.6	122	2	Q9UL84	Q9ul84 homo sapien
15	335	52.5	136	1	HV01_XENLA	P20956 xenopus lae
16	335	52.5	493	2	Q8NCL6	Q8ncl6 homo sapien
17	333.5	52.3	478	2	Q7Z379	Q7z379 homo sapien
18	332	52.0	479	2	Q99M22	Q99m22 mus musculu
19	331	51.9	121	1	HV3J_HUMAN	P01771 homo sapien
20	331	51.9	121	2	Q9UL71	Q9ul71 homo sapien
21	331	51.9	137	1	HV46_MOUSE	P01822 mus musculu

					us-10-631-258-13.rup		
22	329.5	51.6	136	2	Q6LBQ5	Q6lbq5	mus musculu
23	329.5	51.6	465	2	Q6GMX6	Q6gmx6	homo sapien
24	329	51.6	116	2	Q9UL93	Q9ul93	homo sapien
25	328.5	51.5	477	2	Q6GMX7	Q6gmx7	homo sapien
26	327.5	51.3	606	2	Q6GMY2	Q6gmy2	homo sapien
27	327	51.3	499	2	Q8N5K4	Q8n5k4	homo sapien
28	326.5	51.2	119	1	HV38_MOUSE	P01808	mus musculu
29	326.5	51.2	484	2	Q8VEA0	Q8vea0	mus musculu
30	326	51.1	470	2	Q6PJA4	Q6pja4	homo sapien
31	325.5	51.0	112	2	Q9HCC1	Q9hcc1	homo sapien
32	323	50.6	240	2	Q65ZC9	Q65zc9	homo sapien
33	323	50.6	478	2	Q6PI81	Q6pi81	homo sapien
34	322.5	50.5	118	2	Q9UL91	Q9ul91	homo sapien
35	322.5	50.5	576	2	Q6P4I8	Q6p4i8	homo sapien
36	321.5	50.4	473	2	Q91Z05	Q91z05	mus musculu
37	321	50.3	487	2	Q80ZI7	Q80zi7	mus musculu
38	320.5	50.2	119	1	HV40_MOUSE	P01810	mus musculu
39	320	50.2	113	2	Q9UL90	Q9ul90	homo sapien
40	320	50.2	485	2	Q6PDB8	Q6pdb8	mus musculu
41	318.5	49.9	122	1	HV3G_HUMAN	P01768	homo sapien
42	318.5	49.9	475	2	Q6MZQ6	Q6mzq6	homo sapien
43	318	49.8	121	2	Q9UL96	Q9ul96	homo sapien
44	317	49.7	255	2	Q6KB05	Q6kb05	mus musculu
45	316.5	49.6	473	2	Q6MZV7	Q6mzv7	homo sapien

ALIGNMENTS

RESULT 1

HV45_MOUSE

ID HV45_MOUSE STANDARD; PRT; 116 AA.

AC P01821;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region MC101 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=82075900; PubMed=6273429;

RA Kataoka T., Nikaido T., Miyata T., Moriwaki K., Honjo T.;

RT "The nucleotide sequences of rearranged and germline immunoglobulin VH

genes of a mouse myeloma MC101 and evolution of VH genes in mouse.";

RL J. Biol. Chem. 257:277-285(1982).

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; J00502; AAA38515.1; -.

DR PIR; A02096; G1MS10.

DR HSSP; P01820; 1G7J.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

```

DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1      19
FT   CHAIN           20     116      Ig heavy chain V region MC101.
FT   DOMAIN          20    >116      Ig-like.
FT   NON_TER        116     116
SQ   SEQUENCE      116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;

```

```
Qy      1 VKLQESGPGLVQPQSLSITCTVSGFSLTDYGVHWVRQSPGKGLEWLGIWMSGCGTAYTA    60  
       |:|::||| ||||||| | | | | | | | | | | | | | | | | | | | | | |  
Db     21 VQLKQSGPGLVQPQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGIWSGGSTDYNA   80  
  
Qy     61 AFISRLNIYKDNSKNQVFEMNSLQADDTAMYYCAR    96  
       ||||| :| ||||: |||:||| :| ||: ||| |  
Db     81 AFISRLSISKDNSKSQVFFKMNSLQSNDAIYYCAR   116
```

Page 3

us-10-631-258-13.rup

FT	SIGNAL	1	19	
FT	CHAIN	20	144	Ig heavy chain V region MOPC 141.
FT	DOMAIN	20	130	Ig-like.
FT	NON_TER	144	144	
SQ	SEQUENCE	144 AA;	15759 MW;	8E47A7CB3706D30A CRC64;

Query Match 66.6%; Score 425; DB 1; Length 144;
Best Local Similarity 68.5%; Pred. No. 8.5e-36;
Matches 85; Conservative 8; Mismatches 25; Indels 6; Gaps 2;

```

Qy      1 VKLQESGPGLVQPSQSL SITCTVSGFSLTDYGVHWVRQSPGKGLEWLGVIWSGCGTAYTA 60
      |:|:||||| | ||||| ||||| |||:||| ||||| ||| | | :
Db      21 VQLKESGPGLVAPSQSL SITCTVSGFSLTGYGVNWVRQPPGKGLEWLGTIWNGSGTDYNS 80

Qy      61 AFISRLNIYKDNSKNQVFFEMNSLQADDTAMYCCARRGSYPY----NYF--DVWGQGTTV 114
      ||| | |||||:||| :|||| | ||| ||| | | | | | | | | | | | | | | | | |
Db      81 TLKSRLTITKDNSKSQVFLKMNSLQTDDTARYYCASVSIYYYGRSDKYFTLDYWGQGTSV 140

Qy      115 TVSA 118
      |||:
Db      141 TVSS 144

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 15:48:17 ; Search time 2267 Seconds
(without alignments)
2522.151 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGLVQPSQSL SIT.....SYPYNYFDVWGQTTTVTVSA 118

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10631258/runat_07062005_122948_
29497/app_query.fasta_1.263
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10631258 @CGN_1_1_5600 @runat_07062005_122948_29497 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	507.5	79.5	408	10	MUSN	L23131 Mus musculu
2	503	78.8	489	10	AY436968	AY436968 Mus muscu
3	499	78.2	798	6	AR121619	AR121619 Sequence
4	499	78.2	810	6	A41894	A41894 Sequence 2
5	498.5	78.1	345	10	MMU01353	U01353 Mus musculu
6	498.5	78.1	366	10	MMAHCVD	X58292 M.musculus
7	498.5	78.1	450	10	AY436954	AY436954 Mus muscu
8	498	78.1	381	10	MUSIGHLS	J04439 Mouse Ig-mu
9	498	78.1	594	10	S59883	S59883 IgH VDJ [mi
10	497.5	78.0	354	10	MUSIGHMNA	L19122 Mouse Ig re
11	497.5	78.0	1371	6	BD222935	BD222935 Heteromin
12	497.5	78.0	1371	6	AX023359	AX023359 Sequence
13	497.5	78.0	1380	6	CQ856167	CQ856167 Sequence
14	497.5	78.0	1389	6	BD222936	BD222936 Heteromin
15	497.5	78.0	1389	6	AX023361	AX023361 Sequence
16	496.5	77.8	414	10	MMIGG2A	X70822 M.musculus
17	496.5	77.8	492	10	MMU26995	U26995 Mus musculu
18	495.5	77.7	417	10	MUSIHCC	L41878 Mus musculu
19	493	77.3	339	10	AY182545	AY182545 Mus muscu
20	492.5	77.2	419	10	MUSIGMD23A	M27107 Mus musculu
21	491.5	77.0	360	10	AF163756	AF163756 Mus muscu
22	491	77.0	453	10	AY454499	AY454499 Mus muscu
23	490.5	76.9	354	10	AY436943	AY436943 Mus muscu
24	490.5	76.9	384	10	AF072885	AF072885 Mus muscu
25	490	76.8	357	10	MDIGGVAL	Z22047 M.domesticu
26	490	76.8	414	6	AR126845	AR126845 Sequence
27	490	76.8	414	6	I31940	I31940 Sequence 32
28	490	76.8	414	6	I78552	I78552 Sequence 32
29	490	76.8	414	6	I78607	I78607 Sequence 32
30	490	76.8	414	10	MUSABIL2RH	L06840 Mus musculu
31	490	76.8	471	10	MUSIGH1NP	M26981 Mus musculu
32	490	76.8	747	10	S46670	S46670 immunotoxin
33	489	76.6	351	10	AF178587	AF178587 Mus muscu
34	489	76.6	738	10	MMU345034	AJ345034 Mus muscu
35	488.5	76.6	336	10	MUSIGMRNAG	L21022 Mus musculu
36	488.5	76.6	342	6	AR453129	AR453129 Sequence
37	488.5	76.6	342	10	AF287274	AF287274 Mus muscu
38	488.5	76.6	363	10	AY436941	AY436941 Mus muscu
39	488	76.5	369	10	AY550917	AY550917 Mus muscu
40	487	76.3	381	6	I08253	I08253 Sequence 3
41	485.5	76.1	405	10	AF099087	AF099087 Mus muscu
42	484.5	75.9	405	10	AF281861	AF281861 Mus muscu

43	484.5	75.9	1632	12	SYN507107	AJ507107 Synthetic
44	484.5	75.9	1701	12	SCO564232	AJ564232 Synthetic
45	484	75.9	351	10	AY229949	AY229949 Mus muscu

ALIGNMENTS

RESULT 1

MUSN

LOCUS MUSN 408 bp mRNA linear ROD 14-MAR-1994

DEFINITION Mus musculus immunoglobulin heavy chain (IgH) mRNA,VDJ1 region, partial cds.

ACCESSION L23131

VERSION L23131.1 GI:393173

KEYWORDS Ig heavy chain; diversity region; immunoglobulin; joining region; variable region.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 408)

REFERENCE

AUTHORS Sheehan,K.M., Mainville,C.A., Willert,S. and Brodeur,P.H.

TITLE The utilization of individual VH exons in the primary repertoire of

adult BALB/c mice

JOURNAL J. Immunol. 151 (10), 5364-5375 (1993)

MEDLINE 94044761

PUBMED 8228231

COMMENT Original source text: Mus musculus (strain BALB/cByJ) female adult spleen cDNA to mRNA.

FEATURES Location/Qualifiers

source

1. .408
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/cByJ"
/db_xref="taxon:10090"
/map="chromosome 12"
/sex="female"
/cell_type="B-lymphocyte"
/tissue_type="spleen"
/dev_stage="adult"

gene

1. .408
/gene="IgH"

CDS

<1. .>408
/gene="IgH"
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA16775.1"
/db_xref="GI:393174"

/translation="LELLLSLVTFPSCVLSQVQMKQSGPGLVQPSQSL SITCTVSGFS

LTSYGVHWVRQSPGKGLEWLGVWGGSTDYNAAFISRLSISKDNSKSQVFFKMNSLQ

ADDTAIYYCARLGIYYDLWYFDVWGAGTTVTVSS"

V_region

1. .339

ORIGIN

Pred. No.:	1.11e-54	Length:	408
Score:	507.50	Matches:	98
Percent Similarity:	90.00%	Conservative:	10
Best Local Similarity:	81.67%	Mismatches:	9
Query Match:	79.55%	Indels:	3
DB:	10	Gaps:	2

Qy	1	ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	52	GTGCAGATGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	111
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	112	TGCACAGTCTCTGGTTTCTCATTAAGTAGCTATGGTGTACACTGGGTTCGCCAGTCTCCA	171
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	172	GGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGGAAGCACAGACTATAATGCA	231
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	232	GCTTTCATATCCAGACTGAGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTTCTTTAAA	291
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	292	ATGAACAGTCTGCAAGCTGATGACACAGCCATATACTACTGTGCCAGATTGGGAATCTAC	351
Qy	101	ProTyrAsn-----TyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	352	---TATGACCTCTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCCTCA	408

AY436968

LOCUS

LOCUS	AY436968	489 bp	DNA	linear	ROD 15-MAR-
2004					

DEFINITION Mus musculus ZB9D4 ANA immunoglobulin heavy chain gene, partial cds.

ACCESSION AY436968

VERSION AY436968.1 GI:40794884

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 489)
Liang,Z., Xie,C., Chen,C., Kreska,D., Hsu,K., Li,L., Zhou,X.J. and
Mohan,C.

TITLE Pathogenic Profiles and Molecular Signatures of Antinuclear Autoantibodies Rescued from NZM2410 Lupus Mice

JOURNAL J. Exp. Med. 199 (3), 381-398 (2004)

PUBMED 14757744
REFERENCE 2 (bases 1 to 489)
AUTHORS Liang,Z., Xie,C., Chen,C., Kreska,D., Hsu,K., Li,L., Zhou,J.X. and Mohan,C.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-2003) Simmons Arthritis Research Center and Center for Immunology, University of Texas Southwestern Medical School, 5323 Harry Hines Boulevard, Dallas, TX 75390, USA

FEATURES Location/Qualifiers
source 1. .489
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="N2M2410"
/db_xref="taxon:10090"
/chromosome="12"
/cell_line="ZB9D4"
/cell_type="spleen plasma B-cell hybridoma"
/rearranged
mRNA <1. .>489
/product="ANA immunoglobulin heavy chain"
CDS <1. .>489
/note="lupus; anti-DNA; glomerulonephritis"
/codon_start=1
/product="ANA immunoglobulin heavy chain"
/protein_id="AAR90996.1"
/db_xref="GI:40794885"

/translation="VQLQQSGPGLVQPSQSL SITCTVSGFSLTSYGIHWVRQSPGKGL
EWLGVIWSGGSTDYNAPFISRLSISKDNSKSQVFFKMNSLQADDTAIYYCARNFPYGN
FDYWGGGTALTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSG
SCS"

ORIGIN

Alignment Scores:

Pred. No.:	5.19e-54	Length:	489
Score:	503.00	Matches:	94
Percent Similarity:	88.98%	Conservative:	11
Best Local Similarity:	79.66%	Mismatches:	11
Query Match:	78.84%	Indels:	2
DB:	10	Gaps:	1

US-10-631-258-13 (1-118) x AY436968 (1-489)

Qy	1	VallYsLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
		::: :::	
Db	1	GTGCAGCTGCAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	60
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	61	TGCACAGTCTCTGGTTTCTCATTAAGTATGGTATACACTGGGTTCGCCAGTCTCCA	120
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	121	GGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGAAGCACAGACTATAATGCA	180

Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
		::: ::: :::	
Db	181	CCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAAGTTTCTTTAAA	240
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
		::: ::: :::	
Db	241	ATGAACAGTCTGCAAGCTGATGACACAGCCATATATTACTGTGCCAGA-----AATTTT	294
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
		::: :::	
Db	295	CCTTATGGTAACTTCGACTACTGGGGCCAAGGCACCGCTCTCACAGTCTCCTCA	348

us-10-631-258-13.p2n.rng

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 15:43:35 ; Search time 442 Seconds
(without alignments)
1580.383 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGGLVQPSQSLSIT.....SYPYNYFDVWGQTTTVTSA 118

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10631258/runat_07062005_122947_29491/app_query.fasta_1.26
3
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10631258_@CGN_1_1_708_@runat_07062005_122947_29491 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	638	100.0	354	13	ADQ98042	Adq98042 DNA encod
2	638	100.0	681	13	ADQ98068	Adq98068 Chimeric
3	638	100.0	765	13	ADQ98099	Adq98099 Chimeric
4	626	98.1	354	13	ADQ98040	Adq98040 DNA encod
5	626	98.1	681	13	ADQ98066	Adq98066 Chimeric
6	626	98.1	765	13	ADQ98097	Adq98097 Chimeric
7	621	97.3	354	13	ADQ98039	Adq98039 Cloned hy
8	621	97.3	681	13	ADQ98070	Adq98070 Chimeric
9	621	97.3	681	13	ADQ98065	Adq98065 Chimeric
10	621	97.3	765	13	ADQ98101	Adq98101 Chimeric
11	621	97.3	765	13	ADQ98096	Adq98096 Chimeric
12	618	96.9	354	13	ADQ98038	Adq98038 Native hy
13	618	96.9	354	13	ADQ98102	Adq98102 Native hy
14	618	96.9	354	13	ADQ98071	Adq98071 Native hy
15	617	96.7	354	13	ADQ98043	Adq98043 DNA encod
16	617	96.7	354	13	ADQ98041	Adq98041 DNA encod
17	617	96.7	681	13	ADQ98067	Adq98067 Chimeric
18	617	96.7	681	13	ADQ98069	Adq98069 Chimeric
19	617	96.7	765	13	ADQ98098	Adq98098 Chimeric
20	617	96.7	765	13	ADQ98100	Adq98100 Chimeric
21	499	78.2	810	2	AAT27010	Aat27010 Intracell
22	498.5	78.1	348	12	ADQ91073	Adq91073 Anti EpCA
23	498.5	78.1	1479	12	ADQ91081	Adq91081 Antibody
24	498.5	78.1	1479	12	ADQ91105	Adq91105 Antibody
25	498.5	78.1	1479	12	ADQ91079	Adq91079 Bispecifi
26	498.5	78.1	1479	13	ADS99440	Ads99440 Antibody
27	498.5	78.1	1479	13	ADS99446	Ads99446 Antibody
28	498.5	78.1	1479	13	ADS99434	Ads99434 Antibody
29	498.5	78.1	1479	13	ADS99450	Ads99450 Antibody
30	498.5	78.1	1479	13	ADS99430	Ads99430 Antibody
31	498.5	78.1	1479	13	ADS99442	Ads99442 Antibody
32	498.5	78.1	1479	13	ADS99432	Ads99432 Antibody
33	498.5	78.1	1479	13	ADS99444	Ads99444 Antibody
34	498.5	78.1	1479	13	ADS99448	Ads99448 Antibody
35	498.5	78.1	1479	13	ADS99454	Ads99454 Antibody
36	497.5	78.0	1371	3	AAZ50584	Aaz50584 M79scFv-i
37	497.5	78.0	1380	13	ADR43338	Adr43338 scFv anti
38	497.5	78.0	1389	3	AAZ50585	Aaz50585 M79scFv-i
39	493.5	77.4	1479	12	ADQ91091	Adq91091 Antibody
40	490	76.8	414	5	AAF58728	Aaf58728 Murine mi
41	490	76.8	414	12	ADO47748	Ado47748 Mouse mik
42	488.5	76.6	342	6	AAD28602	Aad28602 Escherich
43	484.5	75.9	753	12	ADG28587	Adg28587 Paramyxov
44	484.5	75.9	855	10	ACC57516	Acc57516 Costimula
45	484.5	75.9	1479	12	ADQ91089	Adq91089 Antibody

ALIGNMENTS

RESULT 1
 ADQ98042
 ID ADQ98042 standard; DNA; 354 BP.
 XX
 AC ADQ98042;
 XX
 DT 21-OCT-2004 (first entry)
 XX

us-10-631-258-13.p2n.rng

DE DNA encodes mutant murine antibody 2D12.5 variable heavy chain N87D G54C.

XX
KW murine; mouse; gene; ds; antigen recognition domain; in vivo imaging;
KW cell-antibody-metal chelate complex; emission tomography;
KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW single photon emission tomography; SPET; cancer; cytostatic;
KW immunosuppressive; multi-functional antibody; metal chelate; mutant.

XX
OS Mus musculus.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT CDS 1. .354
FT /*tag= a
FT /partial
FT /product= "Mutant murine 2D12.5 heavy chain variable
FT protein"
FT /note= "Start and stop codons are absent"

XX
PN WO2004065569-A2.

XX
PD 05-AUG-2004.

XX
PF 23-JAN-2004; 2004WO-US001808.

XX
PR 23-JAN-2003; 2003US-00350555.

PR 22-JUL-2003; 2003US-00625047.

PR 31-JUL-2003; 2003US-00631258.

XX
PA (REGC) UNIV CALIFORNIA.

XX
PI Meares C, Corneillie T;

XX
DR WPI; 2004-580725/56.

DR P-PSDB; ADQ98036.

XX
PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.

XX
PS Claim 40; SEQ ID NO 19; 208pp; English.

XX
CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody
CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polynucleotide sequence
CC is the DNA encoding a mutant murine antibody 2D12.5 variable heavy chain

us-10-631-258-13.p2n.rng

CC protein of the invention.

XX

SQ Sequence 354 BP; 83 A; 90 C; 96 G; 85 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5e-63	Length:	354
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98042 (1-354)

```
Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
          |||
Db      1 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 60

Qy     21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
          |||
Db     61 TGCACGGTCTCTGGTTTCTCATTAAGTACTGATGGTGTACACTGGGTTCCGCCAGTCTCCA 120

Qy     41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
          |||
Db    121 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 180

Qy     61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
          |||
Db    181 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA 240

Qy     81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
          |||
Db    241 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 300

Qy    101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
          |||
Db    301 CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354
```

RESULT 2

ADQ98068

ID ADQ98068 standard; DNA; 681 BP.

XX

AC ADQ98068;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric murine N87D G54C 2D12.5 VH antibody fused to human TTCH DNA.

XX

KW murine; mouse; gene; ds; chimeric; human; TTCH; tetanus toxin;
KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW single photon emission tomography; SPET; cancer; cytostatic;
KW immunosuppressive; multi-functional antibody; metal chelate;
KW antigen recognition domain; in vivo imaging;
KW cell-antibody-metal chelate complex; emission tomography; mutant.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 1. .681

FT /*tag= a

us-10-631-258-13.p2n.rng

FT /partial
 FT /product= "Chimeric mutant murine 2D12.5 human anti-
 FT tetanus toxin antibody protein"
 FT /note= "Start and stop codons are absent"
 XX
 PN WO2004065569-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 23-JAN-2004; 2004WO-US001808.
 XX
 PR 23-JAN-2003; 2003US-00350555.
 PR 22-JUL-2003; 2003US-00625047.
 PR 31-JUL-2003; 2003US-00631258.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR P-PSDB; ADQ98061.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 40; SEQ ID NO 45; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polynucleotide sequence
 CC is the DNA encoding a chimeric mutant N87D G54C murine antibody 2D12.5
 CC variable heavy chain protein fused to the human anti-tetanus toxin
 CC antibody CH1 heavy chain constant region of the invention.
 XX
 SQ Sequence 681 BP; 155 A; 208 C; 177 G; 141 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.13e-62	Length:	681
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98068 (1-681)

us-10-631-258-13.p2n.rng

QY 1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
 Db 7 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 66
 QY 21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
 Db 67 TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCCGCCAGTCTCCA 126
 QY 41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
 Db 127 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 186
 QY 61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
 Db 187 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA 246
 QY 81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
 Db 247 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 306
 QY 101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
 Db 307 CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 360

RESULT 3

ADQ98099

ID ADQ98099 standard; DNA; 765 BP.

XX

AC ADQ98099;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric 2dVH-TTCH DNA with tag encoding N87D/G54C mutations SeqID 76.

XX

KW murine; mouse; gene; ds; chimeric; human; TTCH; tetanus toxin;
 KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
 KW single photon emission tomography; SPET; cancer; cytostatic;
 KW immunosuppressive; multi-functional antibody; metal chelate;
 KW antigen recognition domain; in vivo imaging;
 KW cell-antibody-metal chelate complex; emission tomography; V5 epitope;
 KW His tag; mutant.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS

1. .765

FT

/*tag= a

FT

/partial

FT

/product= "Chimeric murine 2D12.5 human anti-tetanus

FT

toxin TTCH antibody protein with V5 epitope and His tag"

FT

/note= "Start codon is absent"

XX

PN WO2004065569-A2.

XX

PD 05-AUG-2004.

XX

PF 23-JAN-2004; 2004WO-US001808.

XX

PR 23-JAN-2003; 2003US-00350555.

us-10-631-258-13.p2n.rng

PR 22-JUL-2003; 2003US-00625047.
PR 31-JUL-2003; 2003US-00631258.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Meares C, Corneillie T;

XX

DR WPI; 2004-580725/56.

DR

P-PSDB; ADQ98106.

XX

PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.

XX

PS Claim 40; SEQ ID NO 76; 208pp; English.

XX

CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody
CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polynucleotide is the
CC mutant DNA sequence encoding a chimeric murine antibody 2D12.5 variable
CC heavy chain protein fused to the human anti-tetanus toxin antibody CH1
CC heavy chain constant region (2dVH-TTCH) with N87D and G54C mutations and
CC a V5 epitope with (His)₆ tag, given in an exemplification of the
CC invention.

XX

SQ Sequence 765 BP; 172 A; 239 C; 192 G; 162 T; 0 U; 0 other;

Alignment Scores:

Pred. No.:	1.31e-62	Length:	765
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98099 (1-765)

Qy	1	ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	7	GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	66
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	67	TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTTCGCCAGTCTCCA	126
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpserGlyCysGlyThrAlaTyrThrAla	60

us-10-631-258-13.p2n.rng

```

Db      127  |||||GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 186
Qy      61  A|a|P|h|e|I|l|e|S|e|r|A|r|g|L|e|u|A|s|n|I|l|e|T|y|r|L|y|s|A|s|n|S|e|r|L|y|s|A|s|n|G|l|n|V|a|l|P|h|e|P|h|e|G|l|u 80
Db      187  |||||GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA 246
Qy      81  M|e|t|A|s|n|S|e|r|L|e|u|G|l|n|A|l|a|A|s|p|A|s|p|T|h|r|A|l|a|M|e|t|T|y|r|T|y|r|C|y|s|A|l|a|A|r|g|A|r|g|G|l|y|S|e|r|T|y|r 100
Db      247  |||||ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 306
Qy      101 P|r|o|T|y|r|A|s|n|T|y|r|P|h|e|A|s|p|V|a|l|T|r|p|G|l|y|G|l|n|G|l|y|T|h|r|T|h|r|V|a|l|T|h|r|V|a|l|S|e|r|A|l|a 118
Db      307  |||||CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 360

```

RESULT 4
ADQ98040

```

ID      ADQ98040 standard; DNA; 354 BP.
XX
AC      ADQ98040;
XX
DT      21-OCT-2004 (first entry)
XX
DE      DNA encoding the mutant murine antibody 2D12.5 variable heavy chain N87D.
XX
KW      murine; mouse; gene; ds; antigen recognition domain; in vivo imaging;
KW      cell-antibody-metal chelate complex; emission tomography;
KW      magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW      single photon emission tomography; SPET; cancer; cytostatic;
KW      immunosuppressive; multi-functional antibody; metal chelate; mutant.
XX
OS      Mus musculus.
OS      Synthetic.
XX
FH      Key          Location/Qualifiers
FT      CDS          1..354
FT                      /*tag= a
FT                      /partial
FT                      /product= "Mutant murine 2D12.5 heavy chain variable
FT                      protein"
FT                      /note= "Start and stop codons are absent"
XX
PN      WO2004065569-A2.
XX
PD      05-AUG-2004.
XX
PF      23-JAN-2004; 2004WO-US001808.
XX
PR      23-JAN-2003; 2003US-00350555.
PR      22-JUL-2003; 2003US-00625047.
PR      31-JUL-2003; 2003US-00631258.
XX
PA      (REGC ) UNIV CALIFORNIA.
XX
PI      Meares C, Corneillie T;
XX
DR      WPI; 2004-580725/56.
DR      P-PSDB; ADQ98034.
XX
PT      Novel mutant antibody comprising reactive site not present in wild-type
PT      of antibody and antigen recognition domain that recognizes macrocyclic
PT      metal chelate having four nitrogen atoms, useful for treating cancer or
PT      autoimmune diseases.

```

XX

PS Claim 40; SEQ ID NO 17; 208pp; English.

XX

CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polynucleotide sequence
 CC is the DNA encoding a mutant murine antibody 2D12.5 variable heavy chain
 CC protein of the invention.

XX

SQ Sequence 354 BP; 85 A; 90 C; 96 G; 83 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.14e-61	Length:	354
Score:	626.00	Matches:	117
Percent Similarity:	99.15%	Conservative:	0
Best Local Similarity:	99.15%	Mismatches:	1
Query Match:	98.12%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98040 (1-354)

```

QY      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      |||
Db      1 GTGAAGCTGCAGGAGTCTGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 60

QY     21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      |||
Db     61 TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCCGCCAGTCTCCA 120

QY     41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      |||
Db    121 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTGGAGGCACGGCCTATACTGCG 180

QY     61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      |||
Db    181 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA 240

QY     81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      |||
Db    241 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 300

QY    101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      |||
Db    301 CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACACGGTCACCGTCTCCGCA 354

```

RESULT 5
 ADQ98066

ID ADQ98066 standard; DNA; 681 BP.
 XX
 AC ADQ98066;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Chimeric murine N87D 2D12.5 VH antibody fused to human TTCH DNA.
 XX
 KW murine; mouse; gene; ds; chimeric; human; TTCH; tetanus toxin;
 KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
 KW single photon emission tomography; SPET; cancer; cytostatic;
 KW immunosuppressive; multi-functional antibody; metal chelate;
 KW antigen recognition domain; in vivo imaging;
 KW cell-antibody-metal chelate complex; emission tomography; mutant.
 XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Chimeric.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .681
 FT /*tag= a
 FT /partial
 FT /product= "Chimeric mutant murine 2D12.5 human anti-
 FT tetanus toxin antibody protein"
 FT /note= "Start and stop codons are absent"
 XX
 PN WO2004065569-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 23-JAN-2004; 2004WO-US001808.
 XX
 PR 23-JAN-2003; 2003US-00350555.
 PR 22-JUL-2003; 2003US-00625047.
 PR 31-JUL-2003; 2003US-00631258.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR P-PSDB; ADQ98059.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 40; SEQ ID NO 43; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody

us-10-631-258-13.p2n.rng

CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polynucleotide sequence
 CC is the DNA encoding a chimeric mutant N87D murine antibody 2D12.5
 CC variable heavy chain protein fused to the human anti-tetanus toxin
 CC antibody CH1 heavy chain constant region of the invention.

XX

SQ Sequence 681 BP; 157 A; 208 C; 177 G; 139 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.58e-61	Length:	681
Score:	626.00	Matches:	117
Percent Similarity:	99.15%	Conservative:	0
Best Local Similarity:	99.15%	Mismatches:	1
Query Match:	98.12%	Indels:	0
DB:	13	Gaps:	0

US-10-631-258-13 (1-118) x ADQ98066 (1-681)

Qy	1	ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	7	GTGAAGCTGCAGGAGTCTGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	66
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	67	TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCCGCCAGTCTCCA	126
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	127	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTGGAGGCACGGCCTATACTGCG	186
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	187	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA	246
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	247	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	306
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118
Db	307	CCTTACAACACTCTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA	360

us-10-631-258-13.p2n.rnpb

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 17:07:34 ; Search time 549 Seconds
(without alignments)
1332.403 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGLVQPSQSL SIT.....SYPYNYFDVWGQTTTVTSA 118

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10631258/runat_07062005_122950_29567/app_query.fasta_1.26
3
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10631258_@CGN_1_1_723_@runat_07062005_122950_29567
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

us-10-631-258-13.p2n.rnpb
 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	638	100.0	354	19	US-10-625-047-19	Sequence 19, Appl
2	638	100.0	354	21	US-10-631-258-19	Sequence 19, Appl
3	638	100.0	354	21	US-10-854-735-19	Sequence 19, Appl
4	638	100.0	354	21	US-10-835-533-19	Sequence 19, Appl
5	638	100.0	681	19	US-10-625-047-45	Sequence 45, Appl
6	638	100.0	681	21	US-10-631-258-45	Sequence 45, Appl
7	626	98.1	354	19	US-10-625-047-17	Sequence 17, Appl
8	626	98.1	354	21	US-10-631-258-17	Sequence 17, Appl
9	626	98.1	354	21	US-10-854-735-17	Sequence 17, Appl
10	626	98.1	354	21	US-10-835-533-17	Sequence 17, Appl
11	626	98.1	681	19	US-10-625-047-43	Sequence 43, Appl
12	626	98.1	681	21	US-10-631-258-43	Sequence 43, Appl
13	621	97.3	354	19	US-10-625-047-16	Sequence 16, Appl
14	621	97.3	354	21	US-10-631-258-16	Sequence 16, Appl
15	621	97.3	354	21	US-10-854-735-16	Sequence 16, Appl
16	621	97.3	354	21	US-10-835-533-16	Sequence 16, Appl
17	621	97.3	681	19	US-10-625-047-42	Sequence 42, Appl
18	621	97.3	681	19	US-10-625-047-47	Sequence 47, Appl
19	621	97.3	681	21	US-10-631-258-42	Sequence 42, Appl
20	621	97.3	681	21	US-10-631-258-47	Sequence 47, Appl
21	618	96.9	354	19	US-10-625-047-15	Sequence 15, Appl
22	618	96.9	354	19	US-10-625-047-48	Sequence 48, Appl
23	618	96.9	354	21	US-10-631-258-15	Sequence 15, Appl
24	618	96.9	354	21	US-10-631-258-48	Sequence 48, Appl
25	618	96.9	354	21	US-10-854-735-15	Sequence 15, Appl
26	618	96.9	354	21	US-10-835-533-15	Sequence 15, Appl
27	617	96.7	354	19	US-10-625-047-18	Sequence 18, Appl
28	617	96.7	354	19	US-10-625-047-20	Sequence 20, Appl
29	617	96.7	354	21	US-10-631-258-18	Sequence 18, Appl
30	617	96.7	354	21	US-10-631-258-20	Sequence 20, Appl
31	617	96.7	354	21	US-10-854-735-18	Sequence 18, Appl
32	617	96.7	354	21	US-10-854-735-20	Sequence 20, Appl
33	617	96.7	354	21	US-10-835-533-18	Sequence 18, Appl
34	617	96.7	354	21	US-10-835-533-20	Sequence 20, Appl
35	617	96.7	681	19	US-10-625-047-44	Sequence 44, Appl
36	617	96.7	681	19	US-10-625-047-46	Sequence 46, Appl
37	617	96.7	681	21	US-10-631-258-44	Sequence 44, Appl
38	617	96.7	681	21	US-10-631-258-46	Sequence 46, Appl
39	498.5	78.1	348	19	US-10-682-845-54	Sequence 54, Appl
40	498.5	78.1	1479	19	US-10-682-845-60	Sequence 60, Appl
41	498.5	78.1	1479	19	US-10-682-845-62	Sequence 62, Appl
42	498.5	78.1	1479	19	US-10-682-845-64	Sequence 64, Appl
43	498.5	78.1	1479	19	US-10-682-845-66	Sequence 66, Appl
44	498.5	78.1	1479	19	US-10-682-845-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-10-625-047-19

; Sequence 19, Application US/10625047

; Publication No. US20040198962A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C

; OTHER INFORMATION: cloned mutant murine 2D12.5 heavy chain variable

; OTHER INFORMATION: region (VH)

US-10-625-047-19

Alignment Scores:

Pred. No.:	3.33e-77	Length:	354
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-10-631-258-13 (1-118) x US-10-625-047-19 (1-354)

Qy	1	VaLLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	1	GTGAAGCTGCAGGAGTCTGGGCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	60
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	61	TGCACGGTCTCTGGTTTCTCATTAAGTACTGACTATGGTGTACACTGGGTTGCGCAGTCTCCA	120
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	121	GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG	180
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	181	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA	240
Qy	81	MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr	100
Db	241	ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC	300
Qy	101	ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla	118

Db 301 CCTTACAACACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354

RESULT 2

US-10-631-258-19

; Sequence 19, Application US/10631258

; Publication No. US20050026263A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130920US

; CURRENT APPLICATION NUMBER: US/10/631,258

; CURRENT FILING DATE: 2003-07-31

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: US 10/625,047

; PRIOR FILING DATE: 2003-07-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C

; OTHER INFORMATION: cloned mutant murine 2D12.5 heavy chain variable

; OTHER INFORMATION: region (VH)

US-10-631-258-19

Alignment Scores:

Pred. No.:	3.33e-77	Length:	354
Score:	638.00	Matches:	118
Percent similarity:	100.00%	Conservative:	0
Best Local similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-631-258-13 (1-118) x US-10-631-258-19 (1-354)

```

QY      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      |||
Db      1 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 60

QY     21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      |||
Db     61 TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTTCGCCAGTCTCCA 120

QY     41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      |||
Db    121 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 180

QY     61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      |||
Db    181 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA 240

QY     81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      |||
Db    241 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 300

QY    101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      |||
Db    301 CCTTACAACACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354

```

RESULT 3

US-10-854-735-19

; Sequence 19, Application US/10854735

; Publication No. US20050042695A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude F.

; APPLICANT: Lebrilla, Carlito B.

; APPLICANT: Butlin, Nathaniel G.

; APPLICANT: Cheal, Sarah M.

; APPLICANT: Corneillie, Todd M.

; APPLICANT: Lee, Susan

; APPLICANT: Whetstone, Paul A.

; APPLICANT: Young, Nicolas L.

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Element-Coded Affinity Tags

; FILE REFERENCE: 023070-136830US

; CURRENT APPLICATION NUMBER: US/10/854,735

; CURRENT FILING DATE: 2004-05-24

; PRIOR APPLICATION NUMBER: US 60/466,529

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: US 60/495,449

; PRIOR FILING DATE: 2003-08-15

; PRIOR APPLICATION NUMBER: US 10/835,533

; PRIOR FILING DATE: 2004-04-28

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:mouse

; OTHER INFORMATION: monoclonal antibody 2D12.5 heavy chain variable

; OTHER INFORMATION: domain (V-H) N87D_G54C cloned sequence

US-10-854-735-19

Alignment Scores:

Pred. No.:	3.33e-77	Length:	354
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-631-258-13 (1-118) x US-10-854-735-19 (1-354)

Qy	1	VaLlYsLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr	20
Db	1	GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC	60
Qy	21	CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro	40
Db	61	TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTTCGCCAGTCTCCA	120
Qy	41	GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla	60
Db	121	GGAAAGGGTCTGGAATGGCTGGGAGTGTATGGAGTGGTTGTGGCACGGCCTATACTGCG	180
Qy	61	AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu	80
Db	181	GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA	240

```

                                us-10-631-258-13.p2n.rnpb
Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354

```

RESULT 4

US-10-835-533-19

```

; Sequence 19, Application US/10835533
; Publication No. US20050059100A1
; GENERAL INFORMATION:
;   APPLICANT: Meares, Claude F.
;   APPLICANT: Whetstone, Paul A.
;   APPLICANT: Corneillie, Todd M.
;   APPLICANT: Butlin, Nathaniel G.
;   APPLICANT: The Regents of the University of California
;   TITLE OF INVENTION: Element-Coded Affinity Tags
;   FILE REFERENCE: 023070-136820US
;   CURRENT APPLICATION NUMBER: US/10/835,533
;   CURRENT FILING DATE: 2004-04-28
;   PRIOR APPLICATION NUMBER: US 60/466,529
;   PRIOR FILING DATE: 2003-04-28
;   PRIOR APPLICATION NUMBER: US 60/495,449
;   PRIOR FILING DATE: 2003-08-15
;   NUMBER OF SEQ ID NOS: 41
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 354
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:mouse
;   OTHER INFORMATION: monoclonal antibody 2D12.5 heavy chain variable
;   OTHER INFORMATION: domain (V-H) N87D_G54C cloned sequence
US-10-835-533-19

```

Alignment Scores:

Pred. No.:	3.33e-77	Length:	354
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-631-258-13 (1-118) x US-10-835-533-19 (1-354)

```

Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTTCGCCAGTCTCCA 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA 240

```

```

Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      |||
Db      241 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 300
      |||
Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      |||
Db      301 CCTTACAACTACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354
      |||

```

RESULT 5

US-10-625-047-45

; Sequence 45, Application US/10625047

; Publication No. US20040198962A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 45

; LENGTH: 681

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D G54C

; OTHER INFORMATION: cloned mutant chimeric murine 2D12.5 heavy chain

; OTHER INFORMATION: variable region (VH) fused to human anti-tetanus

; OTHER INFORMATION: toxin antibody CH1 heavy chain constant region

; OTHER INFORMATION: (TTCH)

US-10-625-047-45

Alignment Scores:

Pred. No.:	7.99e-77	Length:	681
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-10-631-258-13 (1-118) x US-10-625-047-45 (1-681)

```

Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      |||
Db      7 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 66
      |||
Qy      21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      |||
Db      67 TGCACGGTCTCTGGTTTCTCATTAAGTACTGATGGTGTACACTGGGTTTCGCCAGTCTCCA 126
      |||
Qy      41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      |||
Db      127 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 186
      |||
Qy      61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      |||
Db      187 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTCTTTGAA 246
      |||

```

```

                                us-10-631-258-13.p2n.rnpb
Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      247 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 306

Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      307 CCTTACAACACTTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 360

```

RESULT 6

US-10-631-258-45

```

; Sequence 45, Application US/10631258
; Publication No. US20050026263A1
; GENERAL INFORMATION:
;   APPLICANT: Meares, Claude
;   APPLICANT: Corneillie, Todd
;   APPLICANT: The Regents of the University of California
;   TITLE OF INVENTION: Multi-Functional Antibodies
;   FILE REFERENCE: 023070-130920US
;   CURRENT APPLICATION NUMBER: US/10/631,258
;   CURRENT FILING DATE: 2003-07-31
;   PRIOR APPLICATION NUMBER: US 10/350,555
;   PRIOR FILING DATE: 2003-01-23
;   PRIOR APPLICATION NUMBER: US 10/625,047
;   PRIOR FILING DATE: 2003-07-22
;   NUMBER OF SEQ ID NOS: 72
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
;   LENGTH: 681
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:N87D G54C
;   OTHER INFORMATION: cloned mutant, chimeric murine 2D12.5 heavy chain
;   OTHER INFORMATION: variable region (VH) fused to human anti-tetanus
;   OTHER INFORMATION: toxin antibody CH1 heavy chain constant region
;   OTHER INFORMATION: (TTCH)
US-10-631-258-45

```

Alignment Scores:

Pred. No.:	7.99e-77	Length:	681
Score:	638.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-631-258-13 (1-118) x US-10-631-258-45 (1-681)

```

Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 GTGAAGCTGCAGGAGTCTGGGCCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 66

Qy      21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 TGCACGGTCTCTGGTTTCTCATTAAGTACTGATGGTGTACACTGGGTTTCGCCAGTCTCCA 126

Qy      41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      127 GGAAAGGGTCTGGAATGGCTGGGAGTGATATGGAGTGGTTGTGGCACGGCCTATACTGCG 186

Qy      61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      187 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA 246

```

```

Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      |||
Db      247 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 306
      |||
Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
      |||
Db      307 CCTTACAACACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 360
      |||

```

RESULT 7

US-10-625-047-17

; Sequence 17, Application US/10625047

; Publication No. US20040198962A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N87D cloned

; OTHER INFORMATION: mutant murine 2D12.5 heavy chain variable region

; OTHER INFORMATION: (VH)

US-10-625-047-17

Alignment Scores:

Pred. No.:	1.44e-75	Length:	354
Score:	626.00	Matches:	117
Percent Similarity:	99.15%	Conservative:	0
Best Local Similarity:	99.15%	Mismatches:	1
Query Match:	98.12%	Indels:	0
DB:	19	Gaps:	0

US-10-631-258-13 (1-118) x US-10-625-047-17 (1-354)

```

Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      |||
Db      1 GTGAAGCTGCAGGAGTCTGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 60
      |||
Qy      21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      |||
Db      61 TGCACGGTCTCTGGTTTCTCATTAAGTACTATGGTGTACACTGGGTTCCGCCAGTCTCCA 120
      |||
Qy      41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      |||
Db      121 GGAAAGGGTCTGGAATGGCTGGGAGTGTATGGAGTGGTGGAGGCACGGCCTATACTGCG 180
      |||
Qy      61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      |||
Db      181 GCGTTCATATCCAGACTGAACATCTACAAGGACAATTCCAAGAACCAAGTTTTCTTTGAA 240
      |||
Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArgGlySerTyr 100
      |||

```


us-10-631-258-13.p2n.rnpb

```
Db      241 ATGAACAGTCTGCAAGCTGATGACACAGCCATGTATTACTGTGCCAGAAGGGGTAGCTAC 300
Qy      101 ProTyrAsnTyrPheAspValTrpGlyGlnGlyThrThrValThrValSerAla 118
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCTTACAACACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCGCA 354
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 16:01:40 ; Search time 3123 Seconds
(without alignments)
1438.227 Million cell updates/sec

Title: US-10-631-258-13
Perfect score: 638
Sequence: 1 VKLQESGPGGLVQPSQSL SIT.....SYPYNYFDVWGQGT TTVTSA 118

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10631258/runat_07062005_122948_29505/app_query.fasta_1
.263

-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10631258 @CGN_1_1_5180 @runat_07062005_122948_29505 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	485	76.0	480	6	CA577562	CA577562 K0711B09-
2	483.5	75.8	664	6	BY733751	BY733751 BY733751
3	465	72.9	912	5	BU522894	BU522894 AGENCOURT
4	447	70.1	840	4	BI690298	BI690298 603309721
5	446.5	70.0	767	7	CO562905	CO562905 AGENCOURT
6	443.5	69.5	691	2	BF578188	BF578188 602094691
7	441	69.1	671	2	BF182141	BF182141 601804682
8	436.5	68.4	861	5	BU522581	BU522581 AGENCOURT
9	426	66.8	637	2	BF531263	BF531263 602091082
10	425	66.6	742	7	CO567469	CO567469 AGENCOURT
11	425	66.6	793	7	CO574382	CO574382 AGENCOURT
12	423.5	66.4	970	5	BQ940476	BQ940476 AGENCOURT
13	423	66.3	679	6	BY751118	BY751118 BY751118
14	422	66.1	409	6	CB805016	CB805016 AMGNNUC:T
15	416	65.2	368	5	BY221929	BY221929 BY221929
16	414.5	65.0	930	2	BF579344	BF579344 602095631
17	414	64.9	792	7	CO567792	CO567792 AGENCOURT
18	410.5	64.3	520	2	AW917371	AW917371 EST348675
19	407.5	63.9	835	7	CO555748	CO555748 AGENCOURT
20	406	63.6	914	7	CO558560	CO558560 AGENCOURT
21	402	63.0	694	2	BF134274	BF134274 601784250
22	396	62.1	831	7	CO562833	CO562833 AGENCOURT
23	392.5	61.5	881	7	CF592078	CF592078 AGENCOURT
c 24	390	61.1	831	9	CR047446	CR047446 Forward s
25	387	60.7	359	2	BB870665	BB870665 BB870665
26	381.5	59.8	757	7	CF525231	CF525231 AGENCOURT
27	376.5	59.0	717	7	CN823446	CN823446 Oa_splbn_
28	369	57.8	706	7	CK947954	CK947954 4072740 B
29	367	57.5	476	2	BE482206	BE482206 167909 BA
30	367	57.5	626	5	BQ399372	BQ399372 NISC_mp03
31	366.5	57.4	489	2	BE476735	BE476735 160120 BA
32	366.5	57.4	633	5	BQ399193	BQ399193 NISC_mp02
33	364	57.1	492	4	BG692159	BG692159 341738 BA
34	364	57.1	583	2	BE846118	BE846118 232255 BA
35	363	56.9	891	5	BU150876	BU150876 AGENCOURT
36	362.5	56.8	683	7	CN791434	CN791434 4126161 B
37	362	56.7	595	2	BE588903	BE588903 194569 BA
38	361	56.6	547	4	BG692467	BG692467 342167 BA
c 39	361	56.6	685	8	BH275985	BH275985 CH230-96J
40	360.5	56.5	497	2	BE486006	BE486006 173340 BA
41	360.5	56.5	686	7	CK973935	CK973935 4104765 B
42	359.5	56.3	625	7	CV029115	CV029115 7802 Full
43	359.5	56.3	695	4	BG757738	BG757738 602714846
44	359	56.3	549	2	BE845758	BE845758 232868 BA
45	359	56.3	568	7	CO261194	CO261194 4133314 B

ALIGNMENTS

RESULT 1

CA577562

LOCUS CA577562 480 bp mRNA linear EST 19-NOV-2002

DEFINITION K0711B09-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long) Mus musculus cDNA clone NIA:K0711B09 IMAGE:30074612 5', mRNA sequence.

ACCESSION CA577562

VERSION CA577562.1 GI:25125953

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 480)

AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Aiba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.

TITLE Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)

JOURNAL Unpublished (2001)

COMMENT Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

Plate: K0711 row: B column: 09

Seq primer: M13 Reverse

High quality sequence stop: 480

POLYA=No.

FEATURES

source

Location/Qualifiers

1. .480

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6NCr"

/db_xref="niaEST:K0711B09-5N"

/db_xref="taxon:10090"

/clone="NIA:K0711B09 IMAGE:30074612"

/tissue_type="Hematopoietic Stem Cell

(Lin-/c-Kit-/Sca-1-)"

/dev_stage="Age approx.10 weeks old"

/lab_host="DH10B"

/clone_lib="NIA Mouse Hematopoietic Stem Cell

(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"

/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:

NotI; Mouse cDNA project by the Laboratory of Genetics,

National Institute on Aging (NIA), Intramural Research

Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is

a long-transcript enriched cDNA library (Ref. Genome Res.

11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were

obtained from Drs. Dennis Taub, Dan Longo (National

Institute on Aging, USA), Jonathan Keller (National Cancer

Institute, USA). Double-stranded cDNAs were synthesized

with an Oligo(dT) primer [Invitrogen:

5'-pGACTAGTTCTAGATCGCGAGCGGCCCTTTTTTTTTTTTTTTT-3'] from

0.9 ug of total RNA, treated with T4 DNA polymerase, and

purified by ethanol-precipitation. The cDNAs were ligated

to Lone-linker LL-Sal4, purified by phenol/chloroform, and

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 664)

AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasaki, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES Location/Qualifiers
 source 1. .664
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="G630076H03"
 /sex="male"
 /tissue_type="accessory axillary lymph node"
 /dev_stage="adult"
 /clone_lib="RIKEN full-length enriched, adult male
 accessory axillary lymph node"

ORIGIN

Alignment Scores:

Pred. No.:	1.28e-45	Length:	664
Score:	483.50	Matches:	92
Percent Similarity:	84.13%	Conservative:	14
Best Local Similarity:	73.02%	Mismatches:	9
Query Match:	75.78%	Indels:	11
DB:	6	Gaps:	2

US-10-631-258-13 (1-118) x BY733751 (1-664)

```
Qy      1 ValLysLeuGlnGluSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIleThr 20
      |||:::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      92 GTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATAACC 151

Qy      21 CysThrValSerGlyPheSerLeuThrAspTyrGlyValHisTrpValArgGlnSerPro 40
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db     152 TGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTGCCAGTCTCCA 211

Qy      41 GlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyCysGlyThrAlaTyrThrAla 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db     212 GGAAAGGGTCTGGAGTGGCTGGGAGTGATGTGGAGAGGTGGAAGCACAGACTACAATGCA 271

Qy      61 AlaPheIleSerArgLeuAsnIleTyrLysAspAsnSerLysAsnGlnValPhePheGlu 80
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db     272 GCTTTCATGTCCAGACTGAGCATCACCAGGGACAACCTCCAAGAGCCAAGTTTCTTTTAA 331

Qy      81 MetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgArg----- 97
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db     332 ATGAACAGTCTGCAAGCTGATGACACTGCCGTTTACTACTGTGCCAAAATGGGTATGAG 391

Qy      98 -----GlySerTyrProTyrAsnTyrPheAspValTrpGlyGlnGlyThr 112
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

Db 392 AGGGATTACGACGGAGGAACGTAC-----TACTTTGACTACTGGGGCCAAGGCACC 442

Qy 113 ThrValThrValSerAla 118

|||:::|||||:::

Db 443 ACTCTCACAGTCTCCTCA 460